OIPE

RAW SEQUENCE LISTING   DATE: 04/27/2001
PATENT APPLICATION: US/09/832,929   TIME: 13:13:08

Input Set : **A:\PF547SL.txt**
Output Set: **N:\CRF3\04272001\I832929.raw**

ENTERED

see p. 5

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   3 <110> APPLICANT: Rosen, Craig A.
   4        Haseltine, William A.
   6 <120> TITLE OF INVENTION: Albumin Fusion Proteins
   8 <130> FILE REFERENCE: PF547
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/832,929
  11 <141> CURRENT FILING DATE: 2001-04-12
  13 <150> PRIOR APPLICATION NUMBER: 60/229,358
  14 <151> PRIOR FILING DATE: 2000-04-12
  16 <150> PRIOR APPLICATION NUMBER: 60/256,931
  17 <151> PRIOR FILING DATE: 2000-12-21
  19 <150> PRIOR APPLICATION NUMBER: 60/199,384
  20 <151> PRIOR FILING DATE: 2000-04-25
  22 <160> NUMBER OF SEQ ID NOS: 72
  24 <170> SOFTWARE: PatentIn Ver. 2.1
  26 <210> SEQ ID NO: 1
  27 <211> LENGTH: 23
  28 <212> TYPE: DNA
  29 <213> ORGANISM: Artificial Sequence
  31 <220> FEATURE:
  32 <221> NAME/KEY: primer_bind
  33 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
  35 <400> SEQUENCE: 1
  36 cccaagaatt cccttatcca ggc                                        23
  39 <210> SEQ ID NO: 2
  40 <211> LENGTH: 33
  41 <212> TYPE: DNA
  42 <213> ORGANISM: Artificial Sequence
  44 <220> FEATURE:
  45 <221> NAME/KEY: primer_bind
  46 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
  48 <400> SEQUENCE: 2
  49 gggaagctta gaagccacag gatccctcca cag                             33
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  53 <211> LENGTH: 16
  54 <212> TYPE: DNA
  55 <213> ORGANISM: Artificial Sequence
  57 <220> FEATURE:
  58 <221> NAME/KEY: misc_structure
  59 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
  60        with non-cohesive ends.
  62 <400> SEQUENCE: 3
  63 gataaagatt cccaac                                                16
  66 <210> SEQ ID NO: 4
  67 <211> LENGTH: 17
  68 <212> TYPE: DNA
  69 <213> ORGANISM: Artificial Sequence
  71 <220> FEATURE:
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72  <221> NAME/KEY: misc_structure
73  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
74       with non-cohesive ends.
76  <400> SEQUENCE: 4
77  aattgttggg aatcttt                                              17
80  <210> SEQ ID NO: 5
81  <211> LENGTH: 17
82  <212> TYPE: DNA
83  <213> ORGANISM: Artificial Sequence
85  <220> FEATURE:
86  <221> NAME/KEY: misc_structure
87  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
88       with non-cohesive ends.
90  <400> SEQUENCE: 5
91  ttaggcttat tcccaac                                              17
94  <210> SEQ ID NO: 6
95  <211> LENGTH: 18
96  <212> TYPE: DNA
97  <213> ORGANISM: Artificial Sequence
99  <220> FEATURE:
100  <221> NAME/KEY: misc_structure
101  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
102       with non-cohesive ends.
104  <400> SEQUENCE: 6
105  aattgttggg aataagcc                                             18
108  <210> SEQ ID NO: 7
109  <211> LENGTH: 24
110  <212> TYPE: PRT
111  <213> ORGANISM: Artificial Sequence
113  <220> FEATURE:
114  <221> NAME/KEY: SITE
115  <222> LOCATION: 1)..(19)
116  <223> OTHER INFORMATION: invertase leader sequence
118  <220> FEATURE:
119  <221> NAME/KEY: SITE
120  <222> LOCATION: 20)..(24)
121  <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
123  <400> SEQUENCE: 7
124  Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
125    1               5                  10                  15
127  Ile Ser Ala Asp Ala His Lys Ser
128             20
131  <210> SEQ ID NO: 8
132  <211> LENGTH: 21
133  <212> TYPE: DNA
134  <213> ORGANISM: Artificial Sequence
136  <220> FEATURE:
137  <221> NAME/KEY: misc_structure
138  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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```
139         fragments with non-cohesive ends.
141  <400> SEQUENCE: 8
142  gagatgcaca cctgagtgag g                                    21
145  <210> SEQ ID NO: 9
146  <211> LENGTH: 27
147  <212> TYPE: DNA
148  <213> ORGANISM: Artificial Sequence
150  <220> FEATURE:
151  <221> NAME/KEY: misc_structure
152  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
153         fragments with non-cohesive ends.
155  <400> SEQUENCE: 9
156  gatcctgtgg cttcgatgca cacaaga                              27
159  <210> SEQ ID NO: 10
160  <211> LENGTH: 24
161  <212> TYPE: DNA
162  <213> ORGANISM: Artificial Sequence
164  <220> FEATURE:
165  <221> NAME/KEY: misc_structure
166  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
167         fragments with non-cohesive ends.
169  <400> SEQUENCE: 10
170  ctcttgtgtg catcgaagcc acag                                 24
173  <210> SEQ ID NO: 11
174  <211> LENGTH: 30
175  <212> TYPE: DNA
176  <213> ORGANISM: Artificial Sequence
178  <220> FEATURE:
179  <221> NAME/KEY: misc_structure
180  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
181         fragments with non-cohesive ends.
183  <400> SEQUENCE: 11
184  tgtggaagag cctcagaatt tattcccaac                           30
187  <210> SEQ ID NO: 12
188  <211> LENGTH: 31
189  <212> TYPE: DNA
190  <213> ORGANISM: Artificial Sequence
192  <220> FEATURE:
193  <221> NAME/KEY: misc_structure
194  <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
195         fragments with non-cohesive ends.
197  <400> SEQUENCE: 12
198  aattgttggg aataaattct gaggctcttc c                         31
201  <210> SEQ ID NO: 13
202  <211> LENGTH: 47
203  <212> TYPE: DNA
204  <213> ORGANISM: Artificial Sequence
206  <220> FEATURE:
207  <221> NAME/KEY: misc_structure
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208 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
209   fragments with non-cohesive ends.
211 <400> SEQUENCE: 13
212 ttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac   47
215 <210> SEQ ID NO: 14
216 <211> LENGTH: 48
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: misc_structure
222 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
223   fragments with non-cohesive ends.
225 <400> SEQUENCE: 14
226 aattgttggg aaagatccac caccgccgga tccaccgcca cctaagcc   48
229 <210> SEQ ID NO: 15
230 <211> LENGTH: 62
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <221> NAME/KEY: misc_structure
236 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
237   fragments with non-cohesive ends.
239 <400> SEQUENCE: 15
240 ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcggtgg atccttccca 60
241 ac   62
244 <210> SEQ ID NO: 16
245 <211> LENGTH: 63
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <221> NAME/KEY: misc_structure
251 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
252   fragments with non-cohesive ends.
254 <400> SEQUENCE: 16
255 aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60
256 gcc   63
259 <210> SEQ ID NO: 17
260 <211> LENGTH: 1782
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (1)..(1755)
269 <400> SEQUENCE: 17
270 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa   48
271 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
272   1   5   10   15
274 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag   96
275 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln

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```
276              20                25                30
278  cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa   144
279  Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
280          35                40                45
282  ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa   192
283  Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
284      50                55                60
286  tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt   240
287  Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
288  65                70                75                80
290  cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct   288
291  Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
292              85                90                95
294  gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc   336
295  Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
296              100               105               110
298  ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat   384
299  Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
300          115               120               125
302  gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga   432
303  Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
304      130               135               140
306  aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg   480
307  Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
308  145               150               155               160
310  tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc   528
311  Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
312              165               170               175
314  tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg   576
315  Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
316              180               185               190
318  tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa   624
319  Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
320          195               200               205
322  aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc   672
323  Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
324      210               215               220
326  aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa   720
327  Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
328  225               230               235               240
330  gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac   768
331  Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
332              245               250               255
334  agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc   816
335  Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
336              260               265               270
338  agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac   864
339  Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
340          275               280               285
```

**Please Note:**
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 04/27/2001
PATENT APPLICATION: **US/09/832,929**   TIME: 13:13:09

Input Set : **A:\PF547SL.txt**
Output Set: **N:\CRF3\04272001\I832929.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:639 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:644 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:654 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:659 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:664 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:674 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:679 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:684 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:694 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:699 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:704 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:728 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:733 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
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L:748 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:768 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:773 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:778 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:783 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:788 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:793 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:817 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:822 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:827 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:832 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
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L:842 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:847 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:852 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:857 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:862 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:872 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:877 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
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VERIFICATION SUMMARY   DATE: 04/27/2001
PATENT APPLICATION: US/09/832,929   TIME: 13:13:09

        Input Set : A:\PF547SL.txt
        Output Set: N:\CRF3\04272001\I832929.raw

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L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:902 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:907 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:912 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:917 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
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